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RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/777,430A

DATE: 03/25/2002  
TIME: 10:43:00

Input Set : A:\04912-1.txt  
Output Set: N:\CRF3\03252002\I777430A.raw

3 <110> APPLICANT: Lyamichev, Victor  
4 Skrzypczynski, Zbigniew  
5 Allawi, Hatim T.  
6 Wayland, Sarah R.  
7 Takova, Tsetska  
8 Neir, Bruce P.  
10 <120> TITLE OF INVENTION: Charge Tags and the Separation of Nucleic Acid Molecules  
12 <130> FILE REFERENCE: FORS-04912  
14 <140> CURRENT APPLICATION NUMBER: 09/777,430A  
15 <141> CURRENT FILING DATE: 2001-02-06  
17 <160> NUMBER OF SEQ ID NOS: 85  
19 <170> SOFTWARE: PatentIn version 3.1  
21 <210> SEQ ID NO: 1  
22 <211> LENGTH: 21  
23 <212> TYPE: DNA  
24 <213> ORGANISM: Artificial Sequence  
26 <220> FEATURE:  
27 <223> OTHER INFORMATION: Synthetic  
29 <220> FEATURE:  
30 <221> NAME/KEY: misc\_feature  
31 <222> LOCATION: (1)..(2)  
32 <223> OTHER INFORMATION: The residues at these positions are amino-modified bases,  
bearing  
33 a positively charged Cy3 dye.  
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37 tctttcacc agcgagacgg g 21  
40 <210> SEQ ID NO: 2  
41 <211> LENGTH: 23  
42 <212> TYPE: DNA  
43 <213> ORGANISM: Artificial Sequence  
45 <220> FEATURE:  
46 <223> OTHER INFORMATION: Synthetic  
48 <400> SEQUENCE: 2  
49 tattgggcgc cagggtggtt ttt 23  
52 <210> SEQ ID NO: 3  
53 <211> LENGTH: 30  
54 <212> TYPE: DNA  
55 <213> ORGANISM: Artificial Sequence  
57 <220> FEATURE:  
58 <223> OTHER INFORMATION: Synthetic  
60 <400> SEQUENCE: 3  
61 cagggtgaag ggaagaagaa agcgaaaggt 30  
64 <210> SEQ ID NO: 4  
65 <211> LENGTH: 30

## RAW SEQUENCE LISTING

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66 <212> TYPE: DNA  
 67 <213> ORGANISM: Artificial Sequence  
 69 <220> FEATURE:  
 70 <223> OTHER INFORMATION: Synthetic  
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 76 <210> SEQ ID NO: 5  
 77 <211> LENGTH: 28  
 78 <212> TYPE: DNA  
 79 <213> ORGANISM: Artificial Sequence  
 81 <220> FEATURE:  
 82 <223> OTHER INFORMATION: Synthetic  
 84 <400> SEQUENCE: 5  
 85 cacgaattcc gagggcgatgc ttccgctc 28  
 88 <210> SEQ ID NO: 6  
 89 <211> LENGTH: 30  
 90 <212> TYPE: DNA  
 91 <213> ORGANISM: Artificial Sequence  
 93 <220> FEATURE:  
 94 <223> OTHER INFORMATION: Synthetic  
 96 <400> SEQUENCE: 6  
 97 tcgacgtcga ctaacccttg gcggaaagcc 30  
 100 <210> SEQ ID NO: 7  
 101 <211> LENGTH: 23  
 102 <212> TYPE: DNA  
 103 <213> ORGANISM: Artificial Sequence  
 105 <220> FEATURE:  
 106 <223> OTHER INFORMATION: Synthetic  
 108 <400> SEQUENCE: 7  
 109 gcatgcctc ggaattcatg gtc 23  
 112 <210> SEQ ID NO: 8  
 113 <211> LENGTH: 836  
 114 <212> TYPE: PRT  
 115 <213> ORGANISM: Thermus thermophilus  
 117 <400> SEQUENCE: 8  
 119 Met Asn Ser Glu Ala Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val  
 120 1 5 10 15  
 123 Leu Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu  
 124 20 25 30  
 127 Lys Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly  
 128 35 40 45  
 131 Phe Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Tyr Lys Ala  
 132 50 55 60  
 135 Val Phe Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala  
 136 65 70 75 80  
 139 Tyr Glu Ala Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro  
 140 85 90 95  
 143 Arg Gin Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Phe Thr  
 144 100 105 110

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147 Arg Leu Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Thr Leu  
148 115 120 125  
151 Ala Lys Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala  
152 130 135 140  
155 Asp Arg Asp Leu Tyr Gln Leu Val Ser Asp Arg Val Ala Val Leu His  
156 145 150 155 160  
159 Pro Glu Gly His Leu Ile Thr Pro Glu Trp Leu Trp Glu Lys Tyr Gly  
160 165 170 175  
163 Leu Arg Pro Glu Gln Trp Val Asp Phe Arg Ala Leu Val Gly Asp Pro  
164 180 185 190  
167 Ser Asp Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Leu  
168 195 200 205  
171 Lys Leu Leu Lys Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys Asn Leu  
172 210 215 220  
175 Asp Arg Val Lys Pro Glu Asn Val Arg Glu Lys Ile Lys Ala His Leu  
176 225 230 235 240  
179 Glu Asp Leu Arg Leu Ser Leu Glu Leu Ser Arg Val Arg Thr Asp Leu  
180 245 250 255  
183 Pro Leu Glu Val Asp Leu Ala Gln Gly Arg Glu Pro Asp Arg Glu Gly  
184 260 265 270  
187 Leu Arg Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu  
188 275 280 285  
191 Phe Gly Leu Leu Glu Ala Pro Ala Pro Leu Glu Glu Ala Pro Trp Pro  
192 290 295 300  
195 Pro Pro Glu Gly Ala Phe Val Gly Phe Val Leu Ser Arg Pro Glu Pro  
196 305 310 315 320  
199 Met Trp Ala Glu Leu Lys Ala Leu Ala Ala Cys Arg Asp Gly Arg Val  
200 325 330 335  
203 His Arg Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val  
204 340 345 350  
207 Arg Gly Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly  
208 355 360 365  
211 Leu Asp Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu  
212 370 375 380  
215 Asp Pro Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly  
216 385 390 395 400  
219 Glu Trp Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu  
220 405 410 415  
223 His Arg Asn Leu Leu Lys Arg Leu Glu Gly Glu Lys Leu Leu Trp  
224 420 425 430  
227 Leu Tyr His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met  
228 435 440 445  
231 Glu Ala Thr Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser  
232 450 455 460  
235 Leu Glu Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Val Phe Arg  
236 465 470 475 480  
239 Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg  
240 485 490 495  
243 Val Leu Phe Asp Glu Leu Arg Leu Pro Ala Leu Gly Lys Thr Gln Lys

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244	500	505	510
247	Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu		
248	515	520	525
251	Ala His Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys		
252	530	535	540
255	Leu Lys Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg		
256	545	550	555
259	Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly		
260	565	570	575
263	Arg Leu Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr		
264	580	585	590
267	Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp		
268	595	600	605
271	Ala Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala		
272	610	615	620
275	His Leu Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys		
276	625	630	635
279	Asp Ile His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu		
280	645	650	655
283	Ala Val Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly		
284	660	665	670
287	Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile		
288	675	680	685
291	Pro Tyr Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe		
292	690	695	700
295	Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys		
296	705	710	715
299	Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp		
300	725	730	735
303	Leu Asn Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala		
304	740	745	750
307	Phe Asn Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala		
308	755	760	765
311	Met Val Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu		
312	770	775	780
315	Leu Gln Val His Asp Glu Leu Leu Glu Ala Pro Gln Ala Arg Ala		
316	785	790	795
319	Glu Glu Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro		
320	805	810	815
323	Leu Ala Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu		
324	820	825	830
327	Ser Ala Lys Gly		
328	835		
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332	<211> LENGTH: 2511		
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334	<213> ORGANISM: Thermus thermophilus		
336	<400> SEQUENCE: 9		
337	atgaattcccg aggcgatgct tccgctcttt gaacccaaag gccgggtcct cctgggtggac		60

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339	ggccaccacc	tggcttaccg	caccccttc	gccctgaagg	gcctcaccac	gagccggggc	120
341	gaaccgggtgc	aggcggtcta	cggcttcgcc	aagagcctcc	tcaaggccct	gaaggaggac	180
343	gggtacaagg	ccgtcttcgt	ggtctttgac	gccaaaggccc	cctccttcgg	ccacgaggcc	240
345	tacgaggcct	acaaggcggg	gagggccccc	accccccagg	acttccccc	gcagctcgcc	300
347	ctcatcaagg	agctgggtga	cctcctgggg	tttacccgc	tcgaggtccc	cggctacgag	360
349	gcggacgacg	ttctcgccac	cctggccaaag	aaggcgaaa	aggagggta	cgaggtgcgc	420
351	atcctcaccg	ccgaccgcga	cctctaccaa	ctcgctccg	accgcgtcgc	cgtcctccac	480
353	cccgaggggc	acctcatcac	cccgaggtgg	ctttggaga	agtacggct	caggccggag	540
355	cagtgggtgg	acttccgcgc	cctcggtgggg	gaccctccg	acaaccccc	cggggtaaag	600
357	ggcatcgccc	agaagaccgc	cctcaagctc	ctcaaggagt	ggggaaagct	ggaaaacctc	660
359	ctcaagaacc	tggaccgggt	aaagccagaa	aacgtccggg	agaagatcaa	ggcccacctg	720
361	gaagaccta	ggctctcctt	ggagctctcc	cgggtgcga	ccgaccccc	cctggagggtg	780
363	gacctcgccc	aggggcggga	gcccacccgg	gaggggctta	gggccttcct	ggagaggctg	840
365	gagttcggca	gcctcctcca	cgagttcggc	ctccctggagg	cccccgcccc	cctggaggag	900
367	ccccctggc	ccccggccga	agggggccttc	gtgggcttcg	tcctctcccg	ccccgagccc	960
369	atgtggcgg	agcttaaagc	cctggccgccc	tgcagggacg	gcccgggtgca	ccgggcagca	1020
371	gacccttgg	cggggctaaa	ggacctaag	gaggccggg	gcctcctcgc	caaggacctc	1080
373	ggcgcttgg	cctcgaggga	ggggctagac	ctcgccccc	gggacgaccc	catgctcctc	1140
375	gcctacctcc	tggacccttc	caacaccacc	cccgaggggg	tggcgcgcg	ctacgggggg	1200
377	gagtggacgg	aggacgcgc	ccaccggggc	ctccctctcg	agaggctcca	tcgaaacctc	1260
379	cttaagcgcc	tcgagggggg	ggagaagctc	cttggctct	accacgaggt	ggaaaagccc	1320
381	ctctcccggg	tcctggccca	catggaggcc	accggggtac	ggcgggacgt	ggcttacctt	1380
383	caggccctt	ccctggagct	tgcggaggag	atccggccgc	tcgaggagga	ggtcttccgc	1440
385	ttggcgggccc	accccttcaa	cctcaactcc	cgggaccagc	tggaaaggg	gctctttgac	1500
387	gagcttaggc	ttcccgccctt	ggggaaagacg	caaagacag	gcaagcgctc	caccagcgcc	1560
389	gcgggtctgg	aggccctacg	ggaggcccac	cccatcggtg	agaagatct	ccagcaccgg	1620
391	gagctaccca	agctcaagaa	cacctacgtg	gacccttcc	caagcctcg	ccaccccgagg	1680
393	acggggccgccc	tccacacccg	cttcaaccag	acggccacgg	ccacggggag	gcttagtagc	1740
395	tccgacccca	acctgcagaa	catccccgtc	cgcacccccc	tggccagag	gatccggccg	1800
397	gccttcgtgg	ccgaggcgccc	ttgggcgtt	gtggccctgg	actatagcca	gatagagctc	1860
399	cgcgtctcg	cccacctctc	cggggacgaa	aacctgatca	gggtcttcca	ggaggggaag	1920
401	gacatccaca	cccagaccgc	aagctggatg	ttcggcgtcc	ccccggaggg	cgtggacccc	1980
403	ctgatgcgcc	gggcggccaa	gacggtaac	ttcggcgtcc	tctacggcat	gtccgccccat	2040
405	aggctctccc	aggagcttgc	catccccctac	gaggaggccg	tggccttata	agagcgctac	2100
407	ttccaaaggt	tcccaaggt	cggggcctgg	atagaaaaga	ccctggagga	ggggaggaag	2160
409	cggggctacg	tggaaaccct	cttcggaaaga	aggcgctacg	tgcccgcac	caacgccccgg	2220
411	gtgaagagcg	tcagggaggc	cgcggagcgc	atggccttca	acatgcccgt	ccagggcacc	2280
413	gcccgcgacc	tcatgaagct	cgccatgggt	aagcttcc	cccgccctcg	ggagatgggg	2340
415	gcccgcgacc	tcctccaggt	ccacgacgag	ctcctccctgg	aggccccca	agcgcggggcc	2400
417	gaggaggtgg	cggcttggc	caaggaggcc	atggagaagg	cctatccct	cgcgtgccc	2460
419	ctggaggtgg	aggtggggat	ggggaggac	tggcttccg	ccaagggtta	g	2511
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427	<220> FEATURE:						
428	<223> OTHER INFORMATION: Synthetic						
430	<400> SEQUENCE: 10						
431	caggaggagc tcgttgtga cctgga						26

→ Use of n and / or Xaa has been detected in the Sequence Listing. Review the Sequence Listing to ensure a corresponding explanation is present in the <220> to <223> fields of each sequence using n or Xaa.

**VERIFICATION SUMMARY**  
PATENT APPLICATION: **US/09/777,430A**

DATE: 03/25/2002  
TIME: 10:43:01

Input Set : **A:\04912-1.txt**  
Output Set: **N:\CRF3\03252002\I777430A.raw**

L:2453 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:31  
L:2477 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:32  
L:2513 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:34  
L:2543 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:36  
L:2567 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37